

RAW SEQUENCE LISTING

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Application Serial Number: 10/548,748
Source: PCT
Date Processed by STIC: 09/23/2005

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/548,748

DATE: 09/23/2005

TIME: 14:52:53

Input Set : A:\Sequence listing - 12810-00137-US.txt
 Output Set: N:\CRF4\09232005\J548748.raw

3 <110> APPLICANT: Frank, Markus
 4 Kogel, Karl-Heinz
 5 Hueckelhoven, Ralph
 7 <120> TITLE OF INVENTION: METHOD FOR INCREASING RESISTANCE AGAINST STRESS FACTORS IN
 PLANTS
 9 <130> FILE REFERENCE: 12810-00137-US
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/548,748
 C--> 11 <141> CURRENT FILING DATE: 2005-09-08
 11 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/002436
 12 <151> PRIOR FILING DATE: 2004-03-10
 14 <150> PRIOR APPLICATION NUMBER: DE 103 11 118.2
 15 <151> PRIOR FILING DATE: 2003-03-12
 17 <160> NUMBER OF SEQ ID NOS: 63
 19 <170> SOFTWARE: PatentIn version 3.3
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 744
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Hordeum vulgare
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(741)
 29 <223> OTHER INFORMATION: coding for BI1-protein
 31 <400> SEQUENCE: 1
 32 atg gac gcc ttc tac tcg acc tcg tcg gcg gcg gcg agc ggc tgg ggc 48
 33 Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Ala Ala Ser Gly Trp Gly
 34 1 5 10 15
 36 cac gac tcc ctc aag aac ttc cgc cag atc tcc ccc gcc gtg cag tcc 96
 37 His Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val Gln Ser
 38 20 25 30
 40 cac ctc aag ctc gtt tac ctg act cta tgc ttt gca ctg gcc tca tct 144
 41 His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser
 42 35 40 45
 44 gcc gtg ggt gct tac cta cac att gcc ctg aac atc ggc ggg atg ctg 192
 45 Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu
 46 50 55 60
 48 aca atg ctc gct tgt gtc gga act atc gcc tgg atg ttc tcg gtg cca 240
 49 Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro
 50 65 70 75 80
 52 gtc tat gag gag agg aag agg ttt ggg ctg ctg atg ggt gca gcc ctc 288
 53 Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu
 54 85 90 95
 56 ctg gaa ggg gct tcg gtt gga cct ctg att gag ctt gcc ata gac ttt 336
 57 Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe
 58 100 105 110

Cp9-6)

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60 gac cca agc atc ctc gtg aca ggg ttt gtc gga acc gcc atc gcc ttt 384
61 Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
62 115 120 125
64 ggg tgc ttc tct ggc gcc atc atc gcc aag cgc agg gag tac ctg 432
65 Gly Cys Phe Ser Gly Ala Ala Ile Ala Lys Arg Arg Glu Tyr Leu
66 130 135 140
68 tac ctc ggt ggc ctg ctc tct ggc ctg tcg atc ctg ctc tgg ctg 480
69 Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu
70 145 150 155 160
72 cag ttt gtc acg tcc atc ttt ggc cac tcc tct ggc agc ttc atg ttt 528
73 Gln Phe Val Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe
74 165 170 175
76 gag gtt tac ttt ggc ctg ttg atc ttc ctg ggg tac atg gtg tac gac 576
77 Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp
78 180 185 190
80 acg cag gag atc atc gag agg gcg cac cat ggc gac atg gac tac atc 624
81 Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile
82 195 200 205
84 aag cac gcc ctc acc ctc ttc acc gac ttt gtt gcc gtc ctc gtc cga 672
85 Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg
86 210 215 220
88 gtc ctc atc atc atg ctc aag aac gca ggc gac aag tcg gag gac aag 720
89 Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys
90 225 230 235 240
92 aag aag agg aag agg ggg tcc tga 744
93 Lys Lys Arg Lys Arg Gly Ser
94 245
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 247
99 <212> TYPE: PRT
100 <213> ORGANISM: Hordeum vulgare
102 <400> SEQUENCE: 2
103 Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Ala Ala Ser Gly Trp Gly
104 1 5 10 15
106 His Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val Gln Ser
107 20 25 30
109 His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser
110 35 40 45
112 Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu
113 50 55 60
115 Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro
116 65 70 75 80
118 Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu
119 85 90 95
121 Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe
122 100 105 110
124 Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
125 115 120 125
127 Gly Cys Phe Ser Gly Ala Ala Ile Ala Lys Arg Arg Glu Tyr Leu

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128	130	135	140	
130	Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu			
131	145	150	155	160
133	Gln Phe Val Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe			
134	165	170	175	
136	Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp			
137	180	185	190	
139	Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile			
140	195	200	205	
142	Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg			
143	210	215	220	
145	Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys			
146	225	230	235	240
148	Lys Lys Arg Lys Arg Gly Ser			
149	245			
152	<210> SEQ ID NO: 3			
153	<211> LENGTH: 1067			
154	<212> TYPE: DNA			
155	<213> ORGANISM: Arabidopsis thaliana			
157	<220> FEATURE:			
158	<221> NAME/KEY: CDS			
159	<222> LOCATION: (1)..(741)			
160	<223> OTHER INFORMATION: coding for BI1-protein			
162	<400> SEQUENCE: 3			
163	atg gat gcg ttc tct tcc ttc gat tct caa cct ggt agc aga agc	48		
164	Met Asp Ala Phe Ser Ser Phe Phe Asp Ser Gln Pro Gly Ser Arg Ser			
165	1 5 10 15			
167	tgg agc tat gat tct ctt aaa aac ttc cgt cag att tct cca gcc gtt	96		
168	Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val			
169	20 25 30			
171	cag aat cat ctt aaa cgg gtt tat ttg acc tta tgt tgt gct ctt gtg	144		
172	Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val			
173	35 40 45			
175	gcg tct gcc ttt gga gct tac ctc cat gtg ctc tgg aat atc ggc ggt	192		
176	Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly			
177	50 55 60			
179	att ctt aca acg att gga tgt att gga act atg att tgg ctc ctt tca	240		
180	Ile Leu Thr Thr Ile Gly Cys Ile Gly Thr Met Ile Trp Leu Leu Ser			
181	65 70 75 80			
183	tgt cct cct tat gaa cac caa aaa agg ctt tct ctt ctg ttt gtg tct	288		
184	Cys Pro Pro Tyr Glu His Gln Lys Arg Leu Ser Leu Leu Phe Val Ser			
185	85 90 95			
187	gct gtt ctt gaa ggt gct tct gtt ggc ccc ttg atc aaa gtg gca att	336		
188	Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Ile			
189	100 105 110			
191	gat gtt gac cca agc atc ctt atc act gca ttt gtt gga act gcg ata	384		
192	Asp Val Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile			
193	115 120 125			
195	gcg ttt gtc tgt ttc tca gca gca gca atg tta gca aga cgc agg gag	432		

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196 Ala Phe Val Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg Glu
197 130 135 140
199 tat ctc tac ctt gga gga ctg ctt tca tct ggc ttg tct atg cta atg 480
200 Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met
201 145 150 155 160
203 tgg ctc cag ttt gcc tct tca atc ttt ggt ggc tct gca tct atc ttt 528
204 Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe
205 165 170 175
207 aag ttt gag ttg tac ttt gga ctt ttg atc ttt gtg gga tac atg gtg 576
208 Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val
209 180 185 190
211 gtg gac aca caa gag att ata gaa aag gca cac ctc ggt gac atg gac 624
212 Val Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp
213 195 200 205
215 tat gta aaa cat tcg ttg acc ctt ttc act gac ttt gta gct gtg ttt 672
216 Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe
217 210 215 220
219 gtt cgg att ctc atc ata atg ttg aag aac tca gca gat aaa gaa gag 720
220 Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Glu
221 225 230 235 240
223 aag aag aag aaa agg aga aac tgagggatg taaagtaaat ttaactttat 771
224 Lys Lys Lys Arg Arg Asn
225 245
227 ggttgttatac gtgtgtggcc actttgaaga tattacttgt tagcactctc tattgggtac 831
229 cagacatgtt tccactaaaa aggtatctgtt tgtttcattt ctgcacaagt accatcttca 891
231 gattgttaaat gactcgagtg ttgttcttct tttcataaac ttttggcttt taagagttt 951
233 gttctactga ttgcatttcca ccaagctaa aataatgttag gaaaatgata atcctgttta 1011
235 aattttctaa aatgtgtgca tttcagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1067
238 <210> SEQ ID NO: 4
239 <211> LENGTH: 247
240 <212> TYPE: PRT
241 <213> ORGANISM: Arabidopsis thaliana
243 <400> SEQUENCE: 4
244 Met Asp Ala Phe Ser Ser Phe Phe Asp Ser Gln Pro Gly Ser Arg Ser
245 1 5 10 15
247 Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val
248 20 25 30
250 Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val
251 35 40 45
253 Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly
254 50 55 60
256 Ile Leu Thr Thr Ile Gly Cys Ile Gly Thr Met Ile Trp Leu Leu Ser
257 65 70 75 80
259 Cys Pro Pro Tyr Glu His Gln Lys Arg Leu Ser Leu Leu Phe Val Ser
260 85 90 95
262 Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Ile
263 100 105 110
265 Asp Val Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile
266 115 120 125

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268 Ala Phe Val Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg Glu
269 130 135 140
271 Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met
272 145 150 155 160
274 Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe
275 165 170 175
277 Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val
278 180 185 190
280 Val Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp
281 195 200 205
283 Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe
284 210 215 220
286 Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Glu
287 225 230 235 240
289 Lys Lys Lys Arg Arg Asn
290 245
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 1160
295 <212> TYPE: DNA
296 <213> ORGANISM: Nicotiana tabacum
298 <220> FEATURE:
299 <221> NAME/KEY: CDS
300 <222> LOCATION: (1)..(747)
301 <223> OTHER INFORMATION: coding for B11-protein
303 <400> SEQUENCE: 5
304 atg gag tct tgc aca tcg ttc aat tca cag tcg gcg tcg tct cgc 48
305 Met Glu Ser Cys Thr Ser Phe Phe Asn Ser Gln Ser Ala Ser Ser Arg
306 1 5 10 15
308 aat cgc tgg agt tac gat tct ctt aag aac ttc cgc cag atc tct ccc 96
309 Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro
310 20 25 30
312 ttt gtt caa act cat ctc aaa aag gtc tac ctt tca tta tgt tgt gct 144
313 Phe Val Gln Thr His Leu Lys Val Tyr Leu Ser Leu Cys Cys Ala
314 35 40 45
316 tta gtt gct tcg gct gct gga gct tac ctt cac att ctt tgg aac att 192
317 Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile
318 50 55 60
320 ggt ggc tta ctt acg aca ttg gga tgt gtg gga agc ata gtg tgg ctg 240
321 Gly Gly Leu Leu Thr Thr Leu Gly Cys Val Gly Ser Ile Val Trp Leu
322 65 70 75 80
324 atg gcg aca cct ctg tat gaa gag caa aag agg ata gca ctt ctg atg 288
325 Met Ala Thr Pro Leu Tyr Glu Glu Gln Lys Arg Ile Ala Leu Leu Met
326 85 90 95
328 gca gct gca ctg ttt aaa gga gca tct att ggt cca ctg att gaa ttg 336
329 Ala Ala Ala Leu Phe Lys Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu
330 100 105 110
332 gct att gac ttt gac cca agc att gtg atc ggt gct ttt gtt ggt tgt 384
333 Ala Ile Asp Phe Asp Pro Ser Ile Val Ile Gly Ala Phe Val Gly Cys
334 115 120 125

RAW SEQUENCE LISTING ERROR SUMMARY
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DATE: 09/23/2005
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Input Set : A:\Sequence listing - 12810-00137-US.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 1046,1047,1048,1049,1050,1051,1052,1053,1054,1055,1056,1057
Seq#:13; N Pos. 1058,1059,1060,1061,1062,1063,1064,1065,1066,1067,1068,1069
Seq#:13; N Pos. 1070,1071,1072,1073,1074,1075,1076,1077,1078,1079,1080,1081
Seq#:13; N Pos. 1082,1083,1084,1085,1086,1087,1088,1089,1090,1091,1092,1093
Seq#:13; N Pos. 1094,1095
Seq#:34; N Pos. 9590,9764
Seq#:36; N Pos. 9590,9764
Seq#:45; Xaa Pos. 4
Seq#:46; Xaa Pos. 2,6
Seq#:55; Xaa Pos. 4

VERIFICATION SUMMARY
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Input Set : A:\Sequence listing - 12810-00137-US.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:997
M:341 Repeated in SeqNo=13
L:2034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:9540
M:341 Repeated in SeqNo=34
L:2379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:9540
M:341 Repeated in SeqNo=36
L:3092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:3117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:3328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0